CLAIMS

1. A transformant

wherein at least one kind of gene expression cassette comprising a polyester synthesis-associated enzyme gene has been introduced into a yeast.

The transformant according to Claim 1
 wherein the polyester is a copolymer resulting from the
 copolymerization of 3-hydroxyalkanoic acids of the following general formula (1);

in the formula, R represents an alkyl group.

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3. The transformant according to Claim 1 or 2 wherein the polyester is copolyester P(3HB-co-3HH) resulting from the copolymerization of 3-hydroxybutyric acid of the following formula (2) and 3-hydroxyhexanoic acid of the following formula (3);

$$CH_3$$

 $HO-CH-C-C-OH$ (2)

$$\begin{array}{c} C_3H_7 \\ | \\ HO-CH-C-C-OH \\ | H_2 O \end{array}$$
 (3)

The transformant according to any of Claims 1 to 3 wherein the yeast belongs to any of the genera
 Aciculoconidium, Ambrosiozyma, Arthroascus, Arxiozyma, Ashbya, Babjevia, Bensingtonia, Botryoascus, Botryozyma, Brettanomyces,

Bullera, Bulleromyces, Candida, Citeromyces, Clavispora,
Cryptococcus, Cystofilobasidium, Debaryomyces, Dekkara,
Dipodascopsis, Dipodascus, Eeniella, Endomycopsella, Eremascus,
Eremothecium, Erythrobasidium, Fellomyces, Filobasidium,

- Galactomyces, Geotrichum, Guilliermondella, Hanseniaspora,
 Hansenula, Hasegawaea, Holtermannia, Hormoascus, Hyphopichia,
 Issatchenkia, Kloeckera, Kloeckeraspora, Kluyveromyces, Kondoa,
 Kuraishia, Kurtzmanomyces, Leucosporidium, Lipomyces,
 Lodderomyces, Malassezia, Metschnikowia, Mrakia, Myxozyma,
- Nadsonia, Nakazawaea, Nematospora, Ogataea, Oosporidium,
 Pachysolen, Phachytichospora, Phaffia, Pichia, Rhodosporidium,
 Rhodotorula, Saccharomyces, Saccharomycodes, Saccharomycopsis,
 Saitoella, Sakaguchia, Saturnospora, Schizoblastosporion,
 Schizosaccharomyces, Schwanniomyces, Sporidiobolus,
- Sporobolomyces, Sporopachydermia, Stephanoascus, Sterigmatomyces, Sterigmatosporidium, Symbiotaphrina, Sympodiomyces, Sympodiomycopsis, Torulaspora, Trichosporiella, Trichosporon, Trigonopsis, Tsuchiyaea, Udeniomyces, Waltomyces, Wickerhamia, Wickerhamiella, Williopsis, Yamadazyma, Yarrowia,
- 20 Zygoascus, Zygosaccharomyces, Zygowilliopsis and Zygozyma.
 - 5. The transformant according to any of Claims 1 to 4 wherein the yeast is <u>Yarrowia lipolytica</u>.
- 6. The transformant according to any of Claims 1 to 4 wherein the yeast is <u>Candida</u> maltosa.
- The transformant according to any of Claims 1 to 6 wherein a polyester synthesis-associated enzyme gene
 expression cassette comprises a promoter and a terminator, said promoter and said terminator functioning in a yeast.
- 8. The transformant according to Claim 7
 wherein the promoter and terminator are derived from
 35 Yarrowia lipolytica.

9. The transformant according to Claim 7 or 8 wherein the promoter is derived from Yarrowia lipolytica ALK3.

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- 10. The transformant according to Claim 7 or 8 wherein the terminator is derived from Yarrowia lipolytica XPR2.
- 11. The transformant according to Claim 7 wherein the promoter and terminator are derived from Candida maltosa.
- 12. The transformant according to Claim 7 or 11wherein the promoter is derived from Candida maltosa ALK1.
 - 13. The transformant according to Claim 7 or 11 wherein the terminator is derived from $\underline{\text{Candida}}$ $\underline{\text{maltosa}}$ ALK1.

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- 14. The transformant according to any of Claims 1 to 13 wherein the polyester synthesis-associated enzyme gene is derived from <u>Aeromonas</u> caviae.
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 15. The transformant according to any of Claims 1 to 13 wherein the polyester synthesis-associated enzyme gene is a PHA synthase gene derived from Aeromonas caviae or a PHA synthase gene and (R)-specific enoyl-CoA hydratase gene.
- 16. The transformant according to Claim 15
 wherein said PHA synthase gene has the sequence represented
 by SEQ ID NO:3

and the (R)-specific enoyl-CoA hydratase gene has the sequence represented by SEQ ID NO:4.

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17. A method of producing a polyester using the transformant according to any of Claims 1 to 16 which comprises growing said transformant and harvesting a polyester from the resulting culture.

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- 18. A polyester synthesis-associated enzyme gene which is modified from at least one gene code CTG to TTA, TTG, CTT, CTC or CTA.
- 19. The polyester synthesis-associated enzyme gene according to Claim 18

 which codes for an enzyme derived from a bacterium.
- 20. The polyester synthesis-associated enzyme gene according to Claim 19

 wherein said bacterium is Aeromonas caviae.
 - 21. The polyester synthesis-associated enzyme gene according to Claim $20\,$
- wherein the enzyme gene derived from <u>Aeromonas caviae</u> is a PHA synthase gene or a (R)-specific enoyl-CoA hydratase gene.
 - 22. The polyester synthesis-associated enzyme gene according to Claim 21
- wherein said PHA synthase gene has the sequence represented by SEQ ID NO:3.
 - 23. The polyester synthesis-associated enzyme gene according to Claim 21
- wherein said (R)-specific enoyl-CoA hydratase gene has the sequence represented by SEQ ID NO:4.